

“Supplementary Material to “Identification and characterization of repetitive DNA in the genus *Didelphis* Linnaeus, 1758 (*Didelphimorphia*, *Didelphidae*) and the use of satellite DNAs as phylogenetic markers.”

Table S3 - Genome proportion of families of putative satellite DNA in *Didelphis* species and *L. crassicaudata*.

satDNA	Genome proportion (%)							
	<i>D. albiventris</i>	<i>D. aurita</i>	<i>D. imperfecta</i>	<i>D. marsupialis</i>	<i>D. pernigra</i>	<i>D. virginiana</i>	<i>L. crassicaudata</i>	
sat1430	0.0237	0.0062	0.0090	0.0067	0.0018	0.0119	0.0235	
sat206	1.3840*	0.0427	0.8860*	0.1247	0.6593*	0.1886	0.1833	
sat2324	0.1247	0.0881	0.0677	0.0350	0.0447	0.2074	0.4145	
sat907	0.0612	0.0152	0.0438	0.0148	0.0087	0.5917	0.0103	
Total	1.5935	0.1522	1.0064	0.1812	0.7144	0.9996	0.6315	

* genome proportion calculation took into account only the number of reads in the respective satellite cluster (but not the supercluster), which led to a reduced overall satellite DNA proportion when compared to table 1.